Beamline 17-BM / IMCA-CAT

Scientific focus: Pharmaceutical macromolecular crystallography

Scientific programs: Structures of protein–ligand complexes, *de novo* protein structures, drug design, protein engineering, and crystallographic methods development

Optics & Optical Performance

- Daresbury double-crystal constant off-set monochromator
  - 28 m from source
  - 6–20 keV energy range Si(111)
  - 10^{-4} energy resolution ($\Delta E/E$) at 10 keV
  - 35 mm offset below orbital plane
  - water cooling
- sagittally bent 2nd monochromator crystal
- Daresbury vertically focusing mirror
- 3 x 10^{11} ph/sec flux on 200 μm x 200 μm sample at 12.4 keV

Experiment Stations

17-BM-A

- white beam first optics enclosure

17-BM-B

- white/monochromatic beam station
- monochromatic macromolecular crystallography

Detectors

- Mar 165 CCD
- fluorescence detector

Beamline Controls and Data Acquisition

- controls: Sun and Linux systems running EPICS with VME "MX" software (locally developed), running on UNIX
- data acquisition: proprietary software from Mar

Beamline Support Equipment/Facilities

- 4˚ chill room in wet lab
- user-accessible computers for data processing
- Oxford Instruments cryojet for sample cooling

Bending Magnet Source Characteristics (nominal)

source	APS bending magnet
critical energy	19.51 keV
on-axis peak brilliance at 16.3 keV	2.9 x 10^{15} ph/sec/mrad²/mm²/0.1%bw
on-axis peak angular flux at 16.3 keV	9.6 x 10^{13} ph/sec/mrad²/0.1%bw
on-axis peak horizontal angular flux at 5.6 keV	1.6 x 10^{13} ph/sec/mradh/0.1%bw
source size at critical energy Σ_x Σ_y	 145 μm 36 μm
source divergence at critical energy $\Sigma_{x'}$ $\Sigma_{y'}$	 6 mrad 47 μrad